

### **REMARKS**

Claims 112-141, 151-168, 185-216 and 226-243 are currently pending in the application. The foregoing separate sheets marked as "Listing of Claims" show all the claims in the application, with an indication of the current status of each.

Applicant thanks Examiner for the indication in the Office Action dated 10/15/2004 that all claims in the application are allowed. Further to Examiner's comments in that Office Action, Applicant has hereby amended the specification by replacing the first paragraph of the specification with a replacement paragraph that recites that the parent application of the present application is now abandoned and is no longer copending.

Further, Applicant herewith submits a corrected Sequence Listing for the application in which the sequences on page 89 and the sequences on page 69 are listed as SEQ ID NOS: 15 and 16 and SEQ ID NOS: 17 and 18, respectively. In addition, the specification has been amended in order to replace the two paragraphs that contain the sequences, paragraph [0380] on page 89 and paragraph [0329] on page 69, with replacement paragraphs that contain the SEQ ID NOS. Applicant submits that these amendments to the specification do not introduce any new matter, and requests entry of the replacement paragraphs. Applicant notes that the original paragraph [0380] contained underlining in the text within the sequence (the first 23 nucleotides) to indicate the T7 promoter sequence. This underlining has been retained in order to remain true to the original text, and should not be mistaken for new text, even though the new SEQ ID NOS. are also underlined to show that they are being added.

In view of the foregoing, Applicant submits that the application is now in *prima facie* condition for allowance. Should the Examiner find the application to be other than in condition for allowance, the Examiner is requested to contact the undersigned at 703-787-9400 (fax: 703-787-7557; email: ruth@wcc-ip.com) to discuss any other changes deemed necessary in a telephonic or personal interview.

If an extension of time is required for this response to be considered as being timely filed, a conditional petition is hereby made for such extension of time. Please charge any deficiencies in fees and credit any overpayment of fees to Attorney's Deposit Account No. 50-2041.

Respectfully submitted,

A handwritten signature in black ink, appearing to read 'Ruth E. Tyler-Cross', with a large, stylized flourish extending from the end of the signature.

Ruth E. Tyler-Cross  
Reg. No. 45,922

Whitham, Curtis & Christofferson, P.C.  
11491 Sunset Hills Road, Suite 340  
Reston, VA 20190  
703-787-9400  
703-787-7557 (fax)



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

*In re* patent application of Betenbaugh et al.

Serial number: 09/930,440

Group Art Unit: 1652

Attorney Docket Number: 03940077pa

Examiner: Rao

Filed: 2001-08-16

For: ***"ENGINEERING INTRACELLULAR SIALYLATION PATHWAYS"***

SUBMISSION OF SUBSTITUTE SEQUENCE LISTING AND STATEMENT TO SUPPORT  
FILING IN ACCORDANCE WITH 37 C.F.R. § 1.821-1.825

Commissioner for Patents  
P.O. Box 1450  
Alexandria, VA 22313-1450

Dear Sir:

In response to an Office Action mailed 10/15/2004, we enclose herein a corrected substitute computer readable form (diskette) and a corrected substitute paper copy of the sequence listings for the above-identified patent application. Please replace the Sequence Listing of the application with this substitute Sequence Listing. Also enclosed is a verified statement that the content of the paper and computer readable copies are the same and include no new matter.

Respectfully submitted,

Ruth E. Tyler-Cross  
Registration No. 45,922

Whitham, Curtis & Christofferson  
11491 Sunset Hills Road; Suite 340  
Reston, VA 20190  
703-787-9400



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

*In re* patent application of Betenbaugh et al.

Serial number: 09/930,440

Attorney Docket Number: 03940077pa

Filed: 2001-08-16

For: ***"ENGINEERING INTRACELLULAR SIALYLATION PATHWAYS"***

STATEMENT TO SUPPORT FILING AND SUBMISSION IN ACCORDANCE WITH  
37 C.F.R. §§ 1.821-1.825

Assistant Commissioner for Patents  
PO Box 1450  
Alexandria, VA 22313-1450  
**Mail Stop SEQUENCE**

Dear Sir:

In connection with a Substitute Sequence Listing submitted concurrently herewith, the undersigned states that:

1. the submission, filed herewith in accordance with 37 C.F.R. § 1.821 (g), does not include new matter;
2. the content of the attached paper copy and the attached computer readable copy of the Sequence Listing, submitted in accordance with 37 C.F.R. § 1.821(c) and (e), respectively, are the same; and
3. all statements made herein of their own knowledge are true and that all statements made on information and belief are believed to be true; and further, that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that

such willful false statements may jeopardize the validity of the application or any patent resulting therefrom.

Respectfully submitted,

A handwritten signature in black ink, appearing to read "Ruth E. Tyler-Cross", written over a horizontal line.

Ruth E. Tyler-Cross

Reg. No. 45,922

12/09/04

Date



Sequence Listing.ST25.txt  
SEQUENCE LISTING

<110> Betenbaugh, Michael J.  
Lawrence, Shawn J.  
Lee, Yuan C.  
Coleman, Timothy A.

<120> Engineering Intracellular Sialylation Pathways

<130> 03940077pa

<140> 09/930,440

<141> 2001-08-16

<150> US 60/122,582

<151> 1999-03-02

<150> US 60/169,624

<151> 1999-12-08

<150> US 60/227,579

<151> 2000-08-25

<150> US 09/516,793

<151> 2000-03-01

<160> 18

<170> PatentIn version 3.2

<210> 1

<211> 1429

<212> DNA

<213> Homo sapiens

<400> 1

```
atggccttcc caaagaagaa acttcagggt cttgtggctg caaccatcac gccaatgact      60
gagaatggag aaatcaactt ttcagtaatt ggtcagtatg tggattatct tgtgaaagaa      120
cagggagtga agaacatttt tgtgaatggc acaacaggag aaggcctgtc cctgagcgtc      180
tcagagcgtc gccaggttgc agaggagtgg gtgacaaaag ggaaggacaa gctggatcag      240
gtgataattc acgtaggagc actgagcttg aaggagtcac aggaactggc ccaacatgca      300
gcagaaatag gagctgatgg catcgctgtc attgcaccgt tcttcctcaa gccatggacc      360
aaagatatcc tgattaattt cctaaaggaa gtggctgtct cgcgccctgc cctgccattt      420
tattactatc acattcctgc cttgacaggg gtaaagattc gtgctgagga gttgttggat      480
gggattctgg ataagatccc caccttccaa gggctgaaat tcagtatac agatctctta      540
gacttcgggc aatgtgttga tcagaatcgc cagcaacagt ttgctttcct ttttgggggtg      600
gatgagcaac tgttgagtgc tctggtgatg ggagcaactg gagcagtggg cagttttgta      660
tccagagatt tatcaacttt gttgtcaaac taggttttgg agtgtcacag accaaagcca      720
tcatgactct ggtctctggg attccaatgg gccaccccg gcttccactg cagaaagcct      780
ccagggagtt tactgatagt gctgaagcta aactgaagag cctggatttc ctttctttca      840
```

Sequence Listing.ST25.txt

```

ctgatttaaa ggatggaaac ttggaagctg gtagctagtg cctctctatc aaatcagggt      900
ttgcaccttg agacataatc taccttaaata agtgcattttt tttctcaggg aatttttagat      960
gaacttgaat aaactctcct agcaaatgaa atctcacaat aagcattgag gtaccttttg      1020
tgagccttaa aaagtcttat tttgtgaagg ggcaaaaact ctaggagtca caactctcag      1080
tcattcattt cacagattttt tttgtggaga aatttctgtt tatatggatg aaatggaatc      1140
aagaggaaaa ttgtaattga ttaattccat ctgtctttag gagctctcat tatctcggtc      1200
tctggttcct aatcctattt taaagttgtc taattttaaa ccactataat atgtcttcat      1260
tttaataaat attcatttgg aatctaggaa aactctgagc tactgcattt aggcaggcac      1320
tttaataacca aactgtaaca tgtctcaact gtatacaact caaaatacac cagctcattt      1380
ggctgctcag tctaactcta gaatggatgc ttttgaattc atttcgatg      1429

```

<210> 2  
 <211> 304  
 <212> PRT  
 <213> Homo sapiens

<400> 2

Met Ala Phe Pro Lys Lys Lys Leu Gln Gly Leu Val Ala Ala Thr Ile  
 1 5 10 15

Thr Pro Met Thr Glu Asn Gly Glu Ile Asn Phe Ser Val Ile Gly Gln  
 20 25 30

Tyr Val Asp Tyr Leu Val Lys Glu Gln Gly Val Lys Asn Ile Phe Val  
 35 40 45

Asn Gly Thr Thr Gly Glu Gly Leu Ser Leu Ser Val Ser Glu Arg Arg  
 50 55 60

Gln Val Ala Glu Glu Trp Val Thr Lys Gly Lys Asp Lys Leu Asp Gln  
 65 70 75 80

Val Ile Ile His Val Gly Ala Leu Ser Leu Lys Glu Ser Gln Glu Leu  
 85 90 95

Ala Gln His Ala Ala Glu Ile Gly Ala Asp Gly Ile Ala Val Ile Ala  
 100 105 110

Pro Phe Phe Leu Lys Pro Trp Thr Lys Asp Ile Leu Ile Asn Phe Leu  
 115 120 125

Lys Glu Val Ala Ala Ala Ala Pro Ala Leu Pro Phe Tyr Tyr Tyr His  
 130 135 140

Sequence Listing.ST25.txt

Ile Pro Ala Leu Thr Gly Val Lys Ile Arg Ala Glu Glu Leu Leu Asp  
145 150 155 160

Gly Ile Leu Asp Lys Ile Pro Thr Phe Gln Gly Leu Lys Phe Ser Asp  
165 170 175

Thr Asp Leu Leu Asp Phe Gly Gln Cys Val Asp Gln Asn Arg Gln Gln  
180 185 190

Gln Phe Ala Phe Leu Phe Gly Val Asp Glu Gln Leu Leu Ser Ala Leu  
195 200 205

Val Met Gly Ala Thr Gly Ala Val Gly Ser Phe Val Ser Arg Asp Leu  
210 215 220

Ser Thr Leu Leu Ser Asn Val Leu Glu Cys His Arg Pro Lys Pro Ser  
225 230 235 240

Leu Trp Ser Leu Gly Phe Gln Trp Ala His Pro Gly Phe His Cys Arg  
245 250 255

Lys Pro Pro Gly Ser Leu Leu Ile Val Leu Lys Leu Asn Arg Ala Trp  
260 265 270

Ile Ser Phe Leu Ser Leu Ile Arg Met Glu Thr Trp Lys Leu Val Ala  
275 280 285

Ser Ala Ser Leu Ser Asn Gln Gly Phe Ala Pro Leu Arg His Asn Leu  
290 295 300

<210> 3  
<211> 1305  
<212> DNA  
<213> Homo sapiens

<400> 3  
atggactcgg tggagaaggg ggccgccacc tccgtctcca acccgcgggg gcgaccgtcc 60  
cggggccggc cgccgaagct gcagcgcaac tctcgcggcg gccagggccg aggtgtggag 120  
aagccccgc acctggcagc cctaattctg gcccggggag gcagcaaagg catccccctg 180  
aagaacatta agcacctggc ggggggtccc ctcattggct gggtcctgcg tgcggccctg 240  
gattcagggg ccttccagag tgtatgggtt tcgacagacc atgatgaaat tgagaatgtg 300  
gccaaacaat ttggtgcaca agttcatcga agaagttctg aagtttcaaa agacagctct 360  
acctcactag atgccatcat agaatttctt aattatyata atgaggktga cattgtagga 420  
aatattcaag ctacttctyc atgtttacat cctactgatc ttcaaaaagt tgcagaaatg 480



Sequence Listing.ST25.txt

```

attcgagaag aaggatatga ttctgktttc tctgttgtga gacgccatca gtttcgatgg 540
agtgaattc agaaaggagt tcgtgaagt accgaacctc tgaatttaaa tccagctaaa 600
cggcctcgtc gacaagactg ggatggagaa ttatatgaaa atggctcatt ttattttgct 660
aaaagacatt tgatagagat gggttacttg caggggtggaa aaatggcata ctacgaaatg 720
cgagctgaac atagtgtgga tatagatgtg gatattgatt ggcctattgc agagcaaaga 780
gtattaagat atggctatitt tggcaaagag aagcttaagg aaataaaaact tttggtttgc 840
aatattgatg gatgtctcac caatggccac atttatgtat caggagacca aaaagaaata 900
atatcttatg atgtaaaaga tgctattggg ataagtttat taaagaaaag tggatttgag 960
gtgaggctaa tctcagaaag ggcctgttca aagcagacgc tgtcttcttt aaaactggat 1020
tgcaaatgg aagtcagtgt atcagacaag ctagcagttg tagatgaatg gagaaaagaa 1080
atgggcctgt gctggaaaga agtggcatat cttggaaatg aagtgtctga tgaagagtgc 1140
ttgaagagag tgggcctaag tggcgctcct gctgatgcct gttcctacgc ccagaaggct 1200
gttgataca ttgcaaatg taatgggtggc cgtggtgcca tccgagaatt tgcagagcac 1260
atttcctac taatggaaaa agttaataat tcatgccaaa aatag 1305

```

```

<210> 4
<211> 434
<212> PRT
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (133)..(133)
<223> Xaa can be any naturally occurring amino acid

```

```

<220>
<221> misc_feature
<222> (136)..(136)
<223> Xaa can be any naturally occurring amino acid

```

```

<220>
<221> misc_feature
<222> (147)..(147)
<223> Xaa can be any naturally occurring amino acid

```

```

<220>
<221> misc_feature
<222> (169)..(169)
<223> Xaa can be any naturally occurring amino acid

```

```

<400> 4

```

```

Met Asp Ser Val Glu Lys Gly Ala Ala Thr Ser Val Ser Asn Pro Arg
1          5          10          15

```

```

Gly Arg Pro Ser Arg Gly Arg Pro Pro Lys Leu Gln Arg Asn Ser Arg

```

## Sequence Listing.ST25.txt

20

25

30

Gly Gly Gln Gly Arg Gly Val Glu Lys Pro Pro His Leu Ala Ala Leu  
           35                  40                  45  
 Ile Leu Ala Arg Gly Gly Ser Lys Gly Ile Pro Leu Lys Asn Ile Lys  
           50                  55                  60  
 His Leu Ala Gly Val Pro Leu Ile Gly Trp Val Leu Arg Ala Ala Leu  
   65                  70                  75                  80  
 Asp Ser Gly Ala Phe Gln Ser Val Trp Val Ser Thr Asp His Asp Glu  
                   85                  90                  95  
 Ile Glu Asn Val Ala Lys Gln Phe Gly Ala Gln Val His Arg Arg Ser  
                  100                 105                 110  
 Ser Glu Val Ser Lys Asp Ser Ser Thr Ser Leu Asp Ala Ile Ile Glu  
          115                 120                 125  
 Phe Leu Asn Tyr Xaa Asn Glu Xaa Asp Ile Val Gly Asn Ile Gln Ala  
   130                 135                 140  
 Thr Ser Xaa Cys Leu His Pro Thr Asp Leu Gln Lys Val Ala Glu Met  
  145                 150                 155                 160  
 Ile Arg Glu Glu Gly Tyr Asp Ser Xaa Phe Ser Val Val Arg Arg His  
          165                 170                 175  
 Gln Phe Arg Trp Ser Glu Ile Gln Lys Gly Val Arg Glu Val Thr Glu  
          180                 185                 190  
 Pro Leu Asn Leu Asn Pro Ala Lys Arg Pro Arg Arg Gln Asp Trp Asp  
          195                 200                 205  
 Gly Glu Leu Tyr Glu Asn Gly Ser Phe Tyr Phe Ala Lys Arg His Leu  
   210                 215                 220  
 Ile Glu Met Gly Tyr Leu Gln Gly Gly Lys Met Ala Tyr Tyr Glu Met  
  225                 230                 235                 240  
 Arg Ala Glu His Ser Val Asp Ile Asp Val Asp Ile Asp Trp Pro Ile  
          245                 250                 255  
 Ala Glu Gln Arg Val Leu Arg Tyr Gly Tyr Phe Gly Lys Glu Lys Leu  
          260                 265                 270

# Sequence Listing.ST25.txt

Lys Glu Ile Lys Leu Leu Val Cys Asn Ile Asp Gly Cys Leu Thr Asn  
275 280 285

Gly His Ile Tyr Val Ser Gly Asp Gln Lys Glu Ile Ile Ser Tyr Asp  
290 295 300

Val Lys Asp Ala Ile Gly Ile Ser Leu Leu Lys Lys Ser Gly Ile Glu  
305 310 315 320

Val Arg Leu Ile Ser Glu Arg Ala Cys Ser Lys Gln Thr Leu Ser Ser  
325 330 335

Leu Lys Leu Asp Cys Lys Met Glu Val Ser Val Ser Asp Lys Leu Ala  
340 345 350

Val Val Asp Glu Trp Arg Lys Glu Met Gly Leu Cys Trp Lys Glu Val  
355 360 365

Ala Tyr Leu Gly Asn Glu Val Ser Asp Glu Glu Cys Leu Lys Arg Val  
370 375 380

Gly Leu Ser Gly Ala Pro Ala Asp Ala Cys Ser Tyr Ala Gln Lys Ala  
385 390 395 400

Val Gly Tyr Ile Cys Lys Cys Asn Gly Gly Arg Gly Ala Ile Arg Glu  
405 410 415

Phe Ala Glu His Ile Cys Leu Leu Met Glu Lys Val Asn Asn Ser Cys  
420 425 430

Gln Lys

<210> 5  
<211> 1080  
<212> DNA  
<213> Homo sapiens

<400> 5  
atgccgctgg agctggagct gtgtcccggg cgctgggtgg gcgggcaaca cccgtgcttc 60  
atcattgccg agatcggcca gaaccaccag ggcgacctgg acgtagccaa gcgcatgatc 120  
cgcatggcca aggagtgtgg ggctgattgt gccaaagtcc agaagagtga gctagaattc 180  
aagtttaatc ggaaagcctt ggagaggcca tacacctcga agcattcctg ggggaagacg 240  
tacggggagc acaaacgaca tctggagtgc agccatgacc agtacaggga gctgcagagg 300  
tacgccgagg aggttgggat cttcttcact gcctctggca tggatgagat ggcagttgaa 360  
ttcctgcatg aactgaatgt tccatttttc aaagttggat ctggagacac taataatttt 420

Sequence Listing.ST25.txt

```
ccttatctgg aaaagacagc caaaaaaggt cgcccaatgg tgatctccag tgggatgcag 480
tcaatggaca ccatgaagca agtttatcag atcgtgaagc ccctcaaccc caacttctgc 540
ttcttgcaat gtaccagcgc ataccgcgtc cagcctgagg acgtcaacct gcgggtcatc 600
tcggaatatc agaagctctt tcctgacatt cccatagggg attctgggca tgaaacaggc 660
atagcgatat ctgtggccgc agtggctctg ggggccaagg tgttggaaac tcacataact 720
ttggacaaga cctggaaggg gagtgaccac tcggcctcgc tggagcctgg agaactggcc 780
gagctggtgc ggtcagtgcg tcttgtggag cgtgccctgg gctccccaac caagcagctg 840
ctgccctgtg agatggcctg caatgagaag ctgggcaagt ctgtggtggc caaagtgaaa 900
attccggaag gcaccattct aacaatggac atgctcaccg tgaagggtggg tgagcccaaa 960
gcctatcctc ctgaagacat ctttaatcta gtgggcaaga aggtcctggg cactgttgaa 1020
gaggatgaca ccatcatgga agaattggtg gataatcatg gcaaaaaaat caagtcttaa 1080
```

```
<210> 6
<211> 359
<212> PRT
<213> Homo sapiens
```

```
<400> 6
```

```
Met Pro Leu Glu Leu Glu Leu Cys Pro Gly Arg Trp Val Gly Gly Gln
1 5 10 15
```

```
His Pro Cys Phe Ile Ile Ala Glu Ile Gly Gln Asn His Gln Gly Asp
20 25 30
```

```
Leu Asp Val Ala Lys Arg Met Ile Arg Met Ala Lys Glu Cys Gly Ala
35 40 45
```

```
Asp Cys Ala Lys Phe Gln Lys Ser Glu Leu Glu Phe Lys Phe Asn Arg
50 55 60
```

```
Lys Ala Leu Glu Arg Pro Tyr Thr Ser Lys His Ser Trp Gly Lys Thr
65 70 75 80
```

```
Tyr Gly Glu His Lys Arg His Leu Glu Phe Ser His Asp Gln Tyr Arg
85 90 95
```

```
Glu Leu Gln Arg Tyr Ala Glu Glu Val Gly Ile Phe Phe Thr Ala Ser
100 105 110
```

```
Gly Met Asp Glu Met Ala Val Glu Phe Leu His Glu Leu Asn Val Pro
115 120 125
```

Sequence Listing.ST25.txt

Phe Phe Lys Val Gly Ser Gly Asp Thr Asn Asn Phe Pro Tyr Leu Glu  
130 135 140

Lys Thr Ala Lys Lys Gly Arg Pro Met Val Ile Ser Ser Gly Met Gln  
145 150 155 160

Ser Met Asp Thr Met Lys Gln Val Tyr Gln Ile Val Lys Pro Leu Asn  
165 170 175

Pro Asn Phe Cys Phe Leu Gln Cys Thr Ser Ala Tyr Pro Leu Gln Pro  
180 185 190

Glu Asp Val Asn Leu Arg Val Ile Ser Glu Tyr Gln Lys Leu Phe Pro  
195 200 205

Asp Ile Pro Ile Gly Tyr Ser Gly His Glu Thr Gly Ile Ala Ile Ser  
210 215 220

Val Ala Ala Val Ala Leu Gly Ala Lys Val Leu Glu Arg His Ile Thr  
225 230 235 240

Leu Asp Lys Thr Trp Lys Gly Ser Asp His Ser Ala Ser Leu Glu Pro  
245 250 255

Gly Glu Leu Ala Glu Leu Val Arg Ser Val Arg Leu Val Glu Arg Ala  
260 265 270

Leu Gly Ser Pro Thr Lys Gln Leu Leu Pro Cys Glu Met Ala Cys Asn  
275 280 285

Glu Lys Leu Gly Lys Ser Val Val Ala Lys Val Lys Ile Pro Glu Gly  
290 295 300

Thr Ile Leu Thr Met Asp Met Leu Thr Val Lys Val Gly Glu Pro Lys  
305 310 315 320

Ala Tyr Pro Pro Glu Asp Ile Phe Asn Leu Val Gly Lys Lys Val Leu  
325 330 335

Val Thr Val Glu Glu Asp Asp Thr Ile Met Glu Glu Leu Val Asp Asn  
340 345 350

His Gly Lys Lys Ile Lys Ser  
355

<210> 7  
<211> 1059  
<212> DNA

Sequence Listing.ST25.txt

<213> Escherichia coli

<400> 7

atgagtaata tatatatcgt tgctgaaatt ggttgcaacc ataatggtag tgttgatatt	60
gcaagsagaa atgatattaa aagccaaaga ggccggtggt aatgcagtaa aattccaaac	120
atttaaagct gataaattaa tttcagctat tgcacctaag gcagagtatc aaataaaaaa	180
cacaggagaa ttagaatctc agttagaaat gacaaaaaag cttgaaatga agtatgacga	240
ttatctccat ctaatggaat atgcagtcag tttaaattta gatgtttttt ctaccccttt	300
tgacgaagac tctattgatt ttttagcatc tttgaaacaa aaaatatgga aaatcccttc	360
aggtgagtta ttgaatttac cgtatcttga aaaaatagcc aagcttccga tccctgataa	420
gaaaataatc atatcaacag gaatggctac tattgatgag ataaaacagt ctgtttctat	480
ttttataaat aataaagttc cggttggtta tattacaata ttacattgca atactgaata	540
tccaacgccc tttgaggatg taaaccttaa tgctattaat gatttgaaaa aacacttccc	600
taagaataac ataggcttct ctgatcattc tagcgggttt tatgcagcta ttgcggcggt	660
gccttatgga ataactttta ttgaaaaaca ttttacttta gataaatcta tgtctggccc	720
agatcatttg gcctcaatag aacctgatga actgaaacat ctttgtattg gggtcagggtg	780
tgttgaaaaa tctttagggt caaatagtaa agtggttaca gcttcagaaa ggaagaataa	840
aatcgtagca agaaagtcta ttatagctaa acagagataa aaaaagggtga ggttttttca	900
gaaaaaata taacaacaaa aagacctggt aatggatatca gtccgatgga gtggtataat	960
ttattgggta aaattgcaga gcaagacttt attccagatg aattaataat tcatagcgaa	1020
ttcaaaaatc agggggaata atgagaacaa aaattattg	1059

<210> 8

<211> 346

<212> PRT

<213> Escherichia coli

<400> 8

Met	Ser	Asn	Ile	Tyr	Ile	Val	Ala	Glu	Ile	Gly	Cys	Asn	His	Asn	Gly
1				5					10					15	
Ser	Val	Asp	Ile	Ala	Arg	Glu	Met	Ile	Leu	Lys	Ala	Lys	Glu	Ala	Gly
		20						25					30		
Val	Asn	Ala	Val	Lys	Phe	Gln	Thr	Phe	Lys	Ala	Asp	Lys	Leu	Ile	Ser
		35				40						45			
Ala	Ile	Ala	Pro	Lys	Ala	Glu	Tyr	Gln	Ile	Lys	Asn	Thr	Gly	Glu	Leu
	50					55					60				

Sequence Listing.ST25.txt

Glu Ser Gln Leu Glu Met Thr Lys Lys Leu Glu Met Lys Tyr Asp Asp  
 65 70 75 80  
 Tyr Leu His Leu Met Glu Tyr Ala Val Ser Leu Asn Leu Asp Val Phe  
 85 90 95  
 Ser Thr Pro Phe Asp Glu Asp Ser Ile Asp Phe Leu Ala Ser Leu Lys  
 100 105 110  
 Gln Lys Ile Trp Lys Ile Pro Ser Gly Glu Leu Leu Asn Leu Pro Tyr  
 115 120 125  
 Leu Glu Lys Ile Ala Lys Leu Pro Ile Pro Asp Lys Lys Ile Ile Ile  
 130 135 140  
 Ser Thr Gly Met Ala Thr Ile Asp Glu Ile Lys Gln Ser Val Ser Ile  
 145 150 155 160  
 Phe Ile Asn Asn Lys Val Pro Val Gly Asn Ile Thr Ile Leu His Cys  
 165 170 175  
 Asn Thr Glu Tyr Pro Thr Pro Phe Glu Asp Val Asn Leu Asn Ala Ile  
 180 185 190  
 Asn Asp Leu Lys Lys His Phe Pro Lys Asn Asn Ile Gly Phe Ser Asp  
 195 200 205  
 His Ser Ser Gly Phe Tyr Ala Ala Ile Ala Ala Val Pro Tyr Gly Ile  
 210 215 220  
 Thr Phe Ile Glu Lys His Phe Thr Leu Asp Lys Ser Met Ser Gly Pro  
 225 230 235 240  
 Asp His Leu Ala Ser Ile Glu Pro Asp Glu Leu Lys His Leu Cys Ile  
 245 250 255  
 Gly Val Arg Cys Val Glu Lys Ser Leu Gly Ser Asn Ser Lys Val Val  
 260 265 270  
 Thr Ala Ser Glu Arg Lys Asn Lys Ile Val Ala Arg Lys Ser Ile Ile  
 275 280 285  
 Ala Lys Thr Glu Ile Lys Lys Gly Glu Val Phe Ser Glu Lys Asn Ile  
 290 295 300  
 Thr Thr Lys Arg Pro Gly Asn Gly Ile Ser Pro Met Glu Trp Tyr Asn  
 305 310 315 320

# Sequence Listing.ST25.txt

Leu Leu Gly Lys Ile Ala Glu Gln Asp Phe Ile Pro Asp Glu Leu Ile  
 325 330 335

Ile His Ser Glu Phe Lys Asn Gln Gly Glu  
 340 345

<210> 9  
 <211> 20  
 <212> DNA  
 <213> Artificial  
 <220>  
 <223> synthetic oligonucleotide primer: T/C, T, I,  
 C,A,C/T,T,G,G,C,A,C/T,A/T/C,T,I,G,T,I,G,A

<220>  
 <221> misc\_feature  
 <222> (1)..(1)  
 <223> n = t or c

<220>  
 <221> misc\_feature  
 <222> (3)..(3)  
 <223> n = i

<220>  
 <221> misc\_feature  
 <222> (6)..(6)  
 <223> n = c or t

<220>  
 <221> misc\_feature  
 <222> (12)..(12)  
 <223> n = c or t

<220>  
 <221> misc\_feature  
 <222> (13)..(13)  
 <223> n = a, c or t

<220>  
 <221> misc\_feature  
 <222> (15)..(15)  
 <223> n = i

<220>  
 <221> misc\_feature  
 <222> (18)..(18)  
 <223> n = i

<400> 9  
 ntncantggc anntngtnga

20

<210> 10  
 <211> 20  
 <212> DNA  
 <213> Artificial



# Sequence Listing.ST25.txt

<220>  
 <223> synthetic oligonucleotide primer  
 G,A,G/A,A/T,T,A/C/T,G,A,C/T,I,I,I,C,C,I,G,G/C,I,C,A

<220>  
 <221> misc\_feature  
 <222> (3)..(3)  
 <223> n = g or a

<220>  
 <221> misc\_feature  
 <222> (4)..(4)  
 <223> n = a or t

<220>  
 <221> misc\_feature  
 <222> (6)..(6)  
 <223> n = a,c or t

<220>  
 <221> misc\_feature  
 <222> (9)..(9)  
 <223> n = c or t

<220>  
 <221> misc\_feature  
 <222> (10)..(10)  
 <223> n = i

<220>  
 <221> misc\_feature  
 <222> (11)..(11)  
 <223> n = i

<220>  
 <221> misc\_feature  
 <222> (12)..(12)  
 <223> n = i

<220>  
 <221> misc\_feature  
 <222> (15)..(15)  
 <223> n is a, c, g, or t

<220>  
 <221> misc\_feature  
 <222> (17)..(17)  
 <223> n = g or c

<220>  
 <221> misc\_feature  
 <222> (18)..(18)  
 <223> n = i

<400> 10  
 ganntngann nccngnnca

20

<210> 11  
 <211> 20  
 <212> DNA  
 <213> Artificial

# Sequence Listing.ST25.txt

<220>  
 <223> synthetic oligonucleotide primer  
 T,G,I,C/G,C,I,G,G,I,I,I,G/A,T,C,T/G/A,A,T/A,C/T,T,C

<220>  
 <221> misc\_feature  
 <222> (3)..(3)  
 <223> n = i

<220>  
 <221> misc\_feature  
 <222> (4)..(4)  
 <223> n = c or g

<220>  
 <221> misc\_feature  
 <222> (6)..(6)  
 <223> n = i

<220>  
 <221> misc\_feature  
 <222> (9)..(9)  
 <223> n = i

<220>  
 <221> misc\_feature  
 <222> (10)..(10)  
 <223> n = i

<220>  
 <221> misc\_feature  
 <222> (11)..(11)  
 <223> n = i

<220>  
 <221> misc\_feature  
 <222> (12)..(12)  
 <223> n = g or a

<220>  
 <221> misc\_feature  
 <222> (15)..(25)  
 <223> n = t, g or a

<220>  
 <221> misc\_feature  
 <222> (17)..(17)  
 <223> n = t or a

<220>  
 <221> misc\_feature  
 <222> (18)..(18)  
 <223> n = c or t

<400> 11  
 tgnnrngnn nntcnahtc

20

<210> 12  
 <211> 20  
 <212> DNA

Sequence Listing.ST25.txt

<213> Artificial

<220>

<223> synthetic oligonucleotide primer A, C/A/G, C/T,  
T,C,G/A,T,C,I,C,C,I,C,C,I,I,I,G/A,T,G

<220>

<221> misc\_feature

<222> (2)..(2)

<223> n = c, a or g

<220>

<221> misc\_feature

<222> (3)..(3)

<223> n = c or t

<220>

<221> misc\_feature

<222> (6)..(6)

<223> n = g or a

<220>

<221> misc\_feature

<222> (9)..(9)

<223> n = i

<220>

<221> misc\_feature

<222> (12)..(12)

<223> n = i

<220>

<221> misc\_feature

<222> (15)..(15)

<223> n = i

<220>

<221> misc\_feature

<222> (16)..(16)

<223> n = i

<220>

<221> misc\_feature

<222> (17)..(17)

<223> n = i

<220>

<221> misc\_feature

<222> (18)..(18)

<223> n = g or a

<400> 12

anntcttcnc cncnnnntg

20

<210> 13

<211> 54

<212> DNA

<213> Artificial

<220>

<223> synthetic oligonucleotide primer

Sequence Listing.ST25.txt

<400> 13  
tgtaatacga ctactatag ggcggatccg ccatcatgcc gctggagctg gagg 54

<210> 14  
<211> 34  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic oligonucleotide primer

<400> 14  
gtacggtacc ttattaagac ttgatttttt tgcc 34

<210> 15  
<211> 54  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic oligonucleotide primer

<400> 15  
tgtaatacga ctactatag ggcggatccg ccatcatgga ctcggtggag aagg 54

<210> 16  
<211> 44  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic oligonucleotide primer

<400> 16  
gtacggtacc ttactatattt tggcatgaat tattaacttt ttcc 44

<210> 17  
<211> 14  
<212> PRT  
<213> Escherichia coli

<400> 17

Ile Ile Ala Ile Ile Pro Ala Arg Ser Gly Ser Lys Gly Leu  
1 5 10

<210> 18  
<211> 14  
<212> PRT  
<213> Homo sapiens

<400> 18

Leu Ala Ala Leu Ile Leu Ala Arg Gly Gly Ser Lys Gly Ile  
1 5 10